What is claimed is:

1. A substrate having a surface area, the surface area comprising attached labeled probe molecules.

2. The labeled probe molecules of claim 1 wherein label is fluorescent.

3. The labeled probe molecules of claim 1 wherein label fluoresces at a wavelength of about 300 nm to about 700 nm.

4. The substrate of claim 1 wherein the labeled probe molecules are comprised of nucleotides.

5. The labeled probe molecules of claim 2 wherein the nucleotides are nucleotide analogs.

6. The labeled probe molecules of claim 2, wherein the nucleotide analog is 2-amino purine.

7. The substrate of claim 1 wherein the labeled probe molecules are comprised of amino acids.

8. The substrate of claim 1 wherein the labeled probe molecules are comprised of carbohydrates.

9. The substrate of claim 1 wherein the substrate is a microarray.

10. The microarray of claim 9 further having the a surface area divided into quadrants wherein each different quadrant has labeled probe molecules of different sequences.

11. The microarray of claim 9 having from about 100 to about 10,000 different labeled probe molecule sequences located upon about 100 to about 10,000 different quadrants.

12. The microarray of claim 9 having from about 100 to about 1,000 labeled probe molecule per quadrant.

13. The substrate of claim 1 wherein the substrate is a bead.

14. The bead of claim 6 wherein the bead is formed of a ferromagnetic metal core and a polymeric coating.

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15. The bead of claim 7 having from about 100 to about 1,000 labeled probe molecule attached to the surface area of the bead.

16. A method for assessing the presence of a target molecule in a sample comprising the steps of:

a. procuring a microarray having a surface area comprising attached labeled probe molecules in quadrants;

b. detecting the level of label expressed within each quadrant a first time;

c. applying a sample comprising unlabeled nucleotide target sequences to the microarray;

d. providing sufficient conditions and time for target molecules to selectively pair with the labeled probe molecules; and

e. detecting the level of label expressed within each quadrant a second time;

f. comparing the levels of label expressed between the first time and the second time for each quadrant.

17. A method quantifying the amount of a target molecule in a sample comprising the steps of:

a. procuring a first substrate having a surface area comprising a known number of labeled probe molecules;

b. detecting the level of label expressed by the labeled probe molecules on the substrate;

c. contacting a substrate with a volume of sample containing unlabeled target nucleotide sequences;

d. providing sufficient conditions and time for target molecules to selectively pair with the labeled probe molecules;

e. removing the substrate from the sample and detecting the level of label expressed by the substrate after exposure to the sample;

f. where the level of label expression of the first substrate is substantially reduced to levels substantially similar to background levels, repeating steps a. through e. with subsequent substrates, having surface areas comprising a known numbers of labeled probe molecules.

g. Calculating the amount of target molecule in the volume of sample by adding the known number of labeled probe molecules present on the first substrate and subsequent substrates contacted with the sample, wherein the levels of label expression of the substrates were reduced relative to the levels prior to contacting the sample.

18. The method of claim 10, wherein the level of label expression is evaluated using a flow cytometer.

19. A substrate having a surface area divided into quadrants;

different nucleotide probe molecule sequences bound to the surface area, wherein different nucleotide probe molecule sequences are bound to distinct quadrants;

wherein the nucleotide probe molecules are characterized as being a single stranded form or double stranded in form, wherein the level of label expressed from the single stranded probe molecules is greater than the level of label expressed from the double stranded probe molecules; and

wherein the nucleotide probe molecules are further characterized by an ability to hybridize to target nucleotide sequences.